



#114

# SEQUENCE LISTING

<110> MAX-PLANCK-GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN E.V.  
NATIONAL PUBLIC HEALTH INSTITUTE  
PELTONEN, Leena  
AALTONEN, Johanna  
BJORSES, Petra  
PERHEENTUPA, Jaakko  
PALOTIE, Aarno  
HORELLI-KUITUNEN, Nina  
YASPO, Marie-Laure  
LEHRACH, Hans

<120> NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING IN  
MUTATED FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS ECTODERMAL  
DYSTROPHY (APECED)

<130> VOSS1130

<140> US 09/509,595

<141> 2000-07-05

<150> EP 97117154.1

<151> 1997-10-02

<150> EP 97117398.4

<151> 1997-10-08

<150> EP 97119810.6

<151> 1997-11-12

<160> 30

<170> PatentIn version 3.1

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Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr  
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Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu  
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Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His  
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ctg aag gaa aag gag ggc tgc ccc cag gcc ttc cac gcc ctc ctg tcc	312
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Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val	
65 70 75 80	
ctg ttc aag gac tac aac ctg gag cgc tat ggc cgg ctg cag ccc atc	408
Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile	
85 90 95	
ctg gac agc ttc ccc aaa gat gtg gac ctc agc cag ccc cgg aag ggg	456
Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly	
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Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu	
115 120 125	
ccc acc aag agg aag gcc tca gaa gag gct cga gct gcc gcg cca gca	552
Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala	
130 135 140	
gcc ctg act cca agg ggc acc gcc agc cca ggc tct caa ctg aag gcc	600
Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala	
145 150 155 160	
aag ccc ccc aag aag ccg gag agc agc gca gag cag cag cgc ctt cca	648
Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro	
165 170 175	
ctc ggg aac ggg att cag acc atg tca gct tca gtc cag aga gct gtg	696
Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val	
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gcc atg tcc tcc ggg gac gtc ccg gga gcc cga ggg gcc gtg gag ggg	744
Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly	
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Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile	
210 215 220	
cag gtt ggt ggg gag ttc tac act ccc agc aag ttc gaa gac tcc ggc	840
Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly	
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Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val	
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cga gcc aag gga gcc cag ggc gct gcc ccc ggt gga ggt gag gct agg	936
Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg	
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Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp	
275 280 285	
ccc cag ctc cac cag aag aat gag gac gag tgt gcc gtg tgt cgg gac	1032

Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp	
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Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu	
305 310 315 320	
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Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg	
325 330 335	
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Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala	
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Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro	
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Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro	
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cta ctg tgt gtg ggt cct gag ggt cag cag aac ctg gct cct ggt gcg	1416
Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala	
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cgt tgc ggg gtg tgc gga gat ggt acg gac gtg ctg cgg tgt act cac	1464
Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His	
435 440 445	
tgc gcc gct gcc ttc cac tgg cgc tgc cac ttc cca gcc ggc acc tcc	1512
Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser	
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Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr	
465 470 475 480	
cca gcc cct gtg gag ggg gtg ctg gcc ccc agc ccc gcc cgc ctg gcc	1608
Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala	
485 490 495	
cct ggg cct gcc aag gat gac act gcc agt cac gag ccc gct ctg cac	1656
Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His	
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agg gat gac ctg gag tcc ctt ctg agc gag cac acc ttc gat ggc atc	1704
Arg Asp Asp Leu Glu Ser Leu Ser Glu His Thr Phe Asp Gly Ile	
515 520 525	
ctg cag tgg gcc atc cag agc atg gcc cgt ccg gcg gcc ccc ttc ccc	1752
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530 535 540

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 Ser  
 545

acctccttcc tcagtcttgg aagccggccg gctgggatca agaaggggac agcgccacct 1868  
 cttgtcagtg ctgggtgta aacagctctg tgtttctggg gacaccagcc atcatgtgcc 1928  
 tggaaattaa accctgcccc acttctctac tctggaagtc cccgggagcc tctccttgcc 1988  
 tgggtgacct ctaaaaatat aaaaattagc tgggtgtggt ggtgggtgcc tgtaatccca 2048  
 gctacatggg agcctgaggg atgagaatca cttgaactcg ggaggtggag gttgcagtga 2108  
 gctgagattg cgccactgca ctccagtctg gtcggcaaga gtgagactcc gtctcaaaaa 2168  
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 35 40 45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser  
 50 55 60

Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val  
 65 70 75 80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile  
 85 90 95

Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly  
 100 105 110

Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu  
 115 120 125

Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala  
 130 135 140

Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala  
 145 150 155 160

Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro  
 165 170 175

Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val  
 180 185 190

Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly  
 195 200 205

Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile  
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Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly  
 225 230 235 240

Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val  
 245 250 255

Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg  
 260 265 270

Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp  
 275 280 285

Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp  
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Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu  
 305 310 315 320

Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg  
 325 330 335

Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala  
 340 345 350

Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro  
 355 360 365

Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro  
 370 375 380

Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro  
 385 390 395 400

Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro  
 405 410 415

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 420 425 430

Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His  
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Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser  
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Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr  
 465 470 475 480

Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala  
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Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His  
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Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile  
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Ser  
 545

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 acc gag atc gcg gtg gcc ata gac agt gcc ttt ccg ctg ctg cat gct 96  
 Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala  
 20 25 30  
 cta gcc gac cac gac gtg gtc cct gag gac aag ttc cag gag acg ctc 144  
 Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu  
 35 40 45  
 cgt ctg aag gag aag gaa ggc tgc ccc cag gcc ttc cac gcc ctg ctg 192  
 Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu  
 50 55 60  
 tcc tgg ctc ctg acc cgg gac agt ggg gcc atc ctg gat ttc tgg agg 240  
 Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg  
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 att ctc ttt aag gac tac aat ctg gag cgg tac agc cgc ctg cat agc 288  
 Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser

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ggg	aga	aag	ccc	ctt	gct	ggt	ccc	aag	gcc	gcg	gta	ctg	cca	ccc	aga	384
Gly	Arg	Lys	Pro	Leu	Ala	Gly	Pro	Lys	Ala	Ala	Val	Leu	Pro	Pro	Arg	
115								120				125				
ccc	ccc	acc	aag	aga	aaa	gca	ctg	gag	gag	cct	cga	gcc	acc	cca	cca	432
Pro	Pro	Thr	Lys	Arg	Lys	Ala	Leu	Glu	Glu	Pro	Arg	Ala	Thr	Pro	Pro	
130								135				140				
gca	act	ctg	gcc	tca	aag	agc	gtc	tcc	agc	cca	ggc	tcc	cac	ctg	aag	480
Ala	Thr	Leu	Ala	Ser	Lys	Ser	Val	Ser	Ser	Pro	Gly	Ser	His	Leu	Lys	
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act	aag	ccc	cct	aag	aag	cca	gat	ggc	aac	ttg	gag	tca	cag	cac	ctt	528
Thr	Lys	Pro	Pro	Lys	Lys	Pro	Asp	Gly	Asn	Leu	Glu	Ser	Gln	His	Leu	
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cct	ctt	gga	aac	gga	att	cag	acc	atg	gca	gct	tct	gtc	cag	aga	gct	576
Pro	Leu	Gly	Asn	Gly	Ile	Gln	Thr	Met	Ala	Ala	Ser	Val	Gln	Arg	Ala	
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Val	Thr	Val	Ala	Ser	Gly	Asp	Val	Pro	Gly	Thr	Arg	Gly	Ala	Val	Glu	
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ggg	atc	ctt	atc	cag	cag	gtg	ttt	gag	tca	gga	aga	tcc	aag	aag	tgc	672
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agt	ggc	aat	ttg	aag	aac	aag	gcc	cgg	agt	ggt	agc	agc	cta	aag	cca	768
Ser	Gly	Asn	Leu	Lys	Asn	Lys	Ala	Arg	Ser	Gly	Ser	Ser	Leu	Lys	Pro	
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Val	Val	Arg	Ala	Lys	Gly	Ala	Gln	Val	Thr	Ile	Pro	Gly	Arg	Asp	Glu	
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cag	aaa	gtg	ggc	cag	cag	tgt	ggg	gtt	cct	ccc	ctt	cca	tcc	ctc	ccc	864
Gln	Lys	Val	Gly	Gln	Gln	Cys	Gly	Val	Pro	Pro	Leu	Pro	Ser	Leu	Pro	
275								280				285				
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Ser	Glu	Pro	Gln	Val	Asn	Gln	Lys	Asn	Glu	Asp	Glu	Cys	Ala	Val	Cys	
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His	Asp	Gly	Gly	Glu	Leu	Ile	Cys	Cys	Asp	Gly	Cys	Pro	Arg	Ala	Phe	
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His	Leu	Ala	Cys	Leu	Ser	Pro	Pro	Leu	Gln	Glu	Ile	Pro	Ser	Gly	Leu	
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Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile	
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ctc gtg gga ctg agg tca gct tca gag aaa acc agg ggc cca tcc agg	1152
Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg	
370 375 380	
gag ctc aaa gcc agc tct gat gct gct gtc aca tat gtg aac ctg ctg	1200
Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu	
385 390 395 400	
gcc ccg cac cct gca gct cct ctg ctg gag cct tca gca ctg tgc cct	1248
Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro	
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cta ctg agt gct ggg aat gag ggg cgg cca ggt cca gca cca agc gcg	1296
Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala	
420 425 430	
cga tgc agt gtg tgt ggc gat ggc acc gag gtg ttg cgg tgt gca cac	1344
Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His	
435 440 445	
tgt gcc gct gcc ttc cac tgg cgc tgc cac ttc ccg acg gcc gcc gcc	1392
Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala	
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Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr	
465 470 475 480	
ccc acg cca ggc aca ccg ggc gaa gct gta ccc acc tct ggg ccc cgt	1488
Pro Thr Pro Gly Thr Pro Gly Glu Ala Val Pro Thr Ser Gly Pro Arg	
485 490 495	
cca gca cct ggg ctt gcc aag gta ggg gac gac tct gct agt cac gac	1536
Pro Ala Pro Gly Leu Ala Lys Val Gly Asp Asp Ser Ala Ser His Asp	
500 505 510	
cct gtt cta cat agg gac gac ctg gag tcc ctc ctc aat gag cac tca	1584
Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser	
515 520 525	
ttt gac ggc atc ctg cag tgg gcc atc cag agc atg tca cgc ccg ctg	1632
Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ser Arg Pro Leu	
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&lt;213&gt; Murine

&lt;400&gt; 7

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Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu  
 35 40 45

Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu  
 50 55 60

Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg  
 65 70 75 80

Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser  
 85 90 95

Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys  
 100 105 110

Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg  
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Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro  
 130 135 140

Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys  
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Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu  
 165 170 175

Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala  
 180 185 190

Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu  
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Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys  
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Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro

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Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro						
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Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys						
	290		295		300	
His Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe						
305		310		315		320
His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu						
	325		330			335
Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser						
	340		345			350
Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile						
	355		360			365
Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg						
	370		375		380	
Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu						
385		390		395		400
Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro						
	405		410			415
Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala						
	420		425			430
Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His						
	435		440		445	
Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala						
	450		455		460	
Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr						
465		470		475		480

Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu  
115 120 125

Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala  
 130 135 140

Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala  
 145 150 155 160

Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro  
 165 170 175

Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val  
 180 185 190

Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly  
 195 200 205

Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile  
 210 215 220

Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly  
 225 230 235 240

Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val  
 245 250 255

Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg  
 260 265 270

Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp  
 275 280 285

Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp  
 290 295 300

Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu  
 305 310 315 320

Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg  
 325 330 335

Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala  
 340 345 350

Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro  
 355 360 365

Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro

370

375

380

Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro  
 385 390 395 400

Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro  
 405 410 415

Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala  
 420 425 430

Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His  
 435 440 445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser  
 450 455 460

Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr  
 465 470 475 480

Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala  
 485 490 495

Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His  
 500 505 510

Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile  
 515 520 525

Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro  
 530 535 540

Ser  
 545

<210> 9  
 <211> 552  
 <212> PRT  
 <213> Murine

<400> 9

Met Ala Gly Gly Asp Gly Met Leu Arg Arg Leu Leu Arg Leu His Arg  
 1 5 10 15

Thr Glu Ile Ala Val Ala Ile Asp Ser Ala Phe Pro Leu Leu His Ala  
 20 25 30

Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu  
 35 40 45

Arg Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu  
 50 55 60

Ser Trp Leu Leu Thr Arg Asp Ser Gly Ala Ile Leu Asp Phe Trp Arg  
 65 70 75 80

Ile Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Ser Arg Leu His Ser  
 85 90 95

Ile Leu Asp Gly Phe Pro Lys Asp Val Asp Leu Asn Gln Ser Arg Lys  
 100 105 110

Gly Arg Lys Pro Leu Ala Gly Pro Lys Ala Ala Val Leu Pro Pro Arg  
 115 120 125

Pro Pro Thr Lys Arg Lys Ala Leu Glu Glu Pro Arg Ala Thr Pro Pro  
 130 135 140

Ala Thr Leu Ala Ser Lys Ser Val Ser Ser Pro Gly Ser His Leu Lys  
 145 150 155 160

Thr Lys Pro Pro Lys Lys Pro Asp Gly Asn Leu Glu Ser Gln His Leu  
 165 170 175

Pro Leu Gly Asn Gly Ile Gln Thr Met Ala Ala Ser Val Gln Arg Ala  
 180 185 190

Val Thr Val Ala Ser Gly Asp Val Pro Gly Thr Arg Gly Ala Val Glu  
 195 200 205

Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Arg Ser Lys Lys Cys  
 210 215 220

Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Asn Lys Phe Glu Asp Pro  
 225 230 235 240

Ser Gly Asn Leu Lys Asn Lys Ala Arg Ser Gly Ser Ser Leu Lys Pro  
 245 250 255

Val Val Arg Ala Lys Gly Ala Gln Val Thr Ile Pro Gly Arg Asp Glu  
 260 265 270

Gln Lys Val Gly Gln Gln Cys Gly Val Pro Pro Leu Pro Ser Leu Pro  
 275 280 285

Ser Glu Pro Gln Val Asn Gln Lys Asn Glu Asp Glu Cys Ala Val Cys  
 290 295 300

His Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe  
 305 310 315 320

His Leu Ala Cys Leu Ser Pro Pro Leu Gln Glu Ile Pro Ser Gly Leu  
 325 330 335

Trp Arg Cys Ser Cys Cys Leu Gln Gly Arg Val Gln Gln Asn Leu Ser  
 340 345 350

Gln Pro Glu Val Ser Arg Pro Pro Glu Leu Pro Ala Glu Thr Pro Ile  
 355 360 365

Leu Val Gly Leu Arg Ser Ala Ser Glu Lys Thr Arg Gly Pro Ser Arg  
 370 375 380

Glu Leu Lys Ala Ser Ser Asp Ala Ala Val Thr Tyr Val Asn Leu Leu  
 385 390 395 400

Ala Pro His Pro Ala Ala Pro Leu Leu Glu Pro Ser Ala Leu Cys Pro  
 405 410 415

Leu Leu Ser Ala Gly Asn Glu Gly Arg Pro Gly Pro Ala Pro Ser Ala  
 420 425 430

Arg Cys Ser Val Cys Gly Asp Gly Thr Glu Val Leu Arg Cys Ala His  
 435 440 445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Thr Ala Ala Ala  
 450 455 460

Arg Pro Gly Thr Asn Leu Arg Cys Lys Ser Cys Ser Ala Asp Ser Thr  
 465 470 475 480

Pro Thr Pro Gly Thr Pro Gly Glu Ala Val Pro Thr Ser Gly Pro Arg  
 485 490 495

Pro Ala Pro Gly Leu Ala Lys Val Gly Asp Asp Ser Ala Ser His Asp  
 500 505 510

Pro Val Leu His Arg Asp Asp Leu Glu Ser Leu Leu Asn Glu His Ser



515

520

525

Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ser Arg Pro Leu  
 530 535 540

Ala Glu Thr Pro Pro Phe Ser Ser  
 545 550

<210> 10  
 <211> 550  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus sequence of SEQ ID NO:8 & SEQ ID NO:10

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(550)  
 <223> Xaa denotes mismatch of SEQ ID NO:8 & SEQ ID NO:9

<400> 10

Xaa Xaa Xaa Asp Xaa Xaa Leu Arg Arg Leu Leu Arg Leu His Arg Thr  
 1 5 10 15

Glu Ile Ala Val Ala Xaa Asp Ser Ala Phe Pro Leu Leu His Ala Leu  
 20 25 30

Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu Xaa  
 35 40 45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser  
 50 55 60

Trp Leu Leu Thr Xaa Asp Ser Xaa Ala Ile Leu Asp Phe Trp Arg Xaa  
 65 70 75 80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Xaa Arg Leu Xaa Xaa Ile  
 85 90 95

Leu Asp Xaa Phe Pro Lys Asp Val Asp Leu Xaa Gln Xaa Arg Lys Gly  
 100 105 110

Arg Lys Pro Xaa Ala Xaa Pro Lys Ala Xaa Val Xaa Pro Pro Arg Xaa  
 115 120 125

Pro Thr Lys Arg Lys Ala Xaa Glu Glu Xaa Arg Ala Xaa Xaa Pro Ala  
 130 135 140

Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Ser Pro Gly Ser Xaa Leu Lys Xaa  
 145 150 155 160

Lys Pro Pro Lys Lys Pro Xaa Xaa Xaa Xaa Glu Xaa Gln Xaa Leu Pro  
 165 170 175

Leu Gly Asn Gly Ile Gln Thr Met Xaa Ala Ser Val Gln Arg Ala Val  
 180 185 190

Xaa Xaa Xaa Ser Gly Asp Val Pro Gly Xaa Arg Gly Ala Val Glu Gly  
 195 200 205

Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Xaa Ser Lys Lys Cys Ile  
 210 215 220

Gln Val Gly Gly Glu Phe Tyr Thr Pro Xaa Lys Phe Glu Asp Xaa Ser  
 225 230 235 240

Gly Xaa Xaa Lys Asn Lys Ala Arg Ser Xaa Ser Xaa Xaa Lys Pro Xaa  
 245 250 255

Val Arg Ala Lys Gly Ala Gln Xaa Xaa Xaa Pro Gly Xaa Xaa Glu Xaa  
 260 265 270

Xaa Xaa Gly Gln Gln Xaa Xaa Val Pro Xaa Xaa Xaa Xaa Leu Pro Ser  
 275 280 285

Xaa Pro Gln Xaa Xaa Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Xaa  
 290 295 300

Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His  
 305 310 315 320

Leu Ala Cys Leu Ser Pro Pro Leu Xaa Glu Ile Pro Ser Gly Xaa Trp  
 325 330 335

Arg Cys Ser Xaa Cys Leu Gln Xaa Xaa Val Gln Xaa Xaa Xaa Xaa Xaa  
 340 345 350

Xaa Glu Xaa Xaa Arg Pro Xaa Glu Xaa Pro Xaa Glu Thr Pro Xaa Xaa  
 355 360 365

Xaa Gly Leu Arg Ser Ala Xaa Glu Xaa Xaa Arg Gly Pro Xaa Xaa Glu  
 370 375 380

Xaa Xaa Ala Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Xaa Xaa Leu Xaa Ala  
 385 390 395 400

Pro Xaa Xaa Ala Ala Pro Leu Xaa Xaa Leu Xaa Xaa Ser Ala Leu Xaa  
 405 410 415

Pro Leu Leu Xaa Xaa Gly Xaa Glu Gly Xaa Xaa Xaa Xaa Ala Pro Xaa  
 420 425 430

Ala Arg Cys Xaa Val Cys Gly Asp Gly Thr Xaa Val Leu Arg Cys Xaa  
 435 440 445

His Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Xaa Xaa Xaa  
 450 455 460

Xaa Arg Pro Gly Thr Xaa Leu Arg Cys Xaa Ser Cys Ser Xaa Asp Xaa  
 465 470 475 480

Thr Pro Xaa Pro Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Ser Xaa Xaa  
 485 490 495

Arg Xaa Ala Pro Gly Xaa Ala Lys Xaa Xaa Asp Asp Xaa Ala Ser His  
 500 505 510

Xaa Pro Xaa Leu His Arg Asp Asp Leu Glu Ser Leu Leu Xaa Glu His  
 515 520 525

Xaa Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Xaa Arg Pro  
 530 535 540

Xaa Ala Xaa Xaa Pro Xaa  
 545 550

<210> 11  
 <211> 48  
 <212> DNA  
 <213> Mouse

<400> 11  
 ggggcctcga tggacgtctc tggggcccag gtcgtgggtc gcgcgcta

48

<210> 12  
 <211> 15  
 <212> PRT  
 <213> Mouse

<400> 12

Pro Glu Leu Pro Ala Glu Thr Pro Gly Pro Ala Pro Ser Ala Arg

1 5 10 15

<210> 13  
 <211> 43  
 <212> DNA  
 <213> Mouse

<400> 13  
 agtgagcccc aggttaacca gaacgaggat gagtgtgccg tgt 43

<210> 14  
 <211> 14  
 <212> PRT  
 <213> Mouse

<400> 14

Ser Glu Pro Gln Val Asn Gln Asn Glu Asp Glu Cys Ala Val  
 1 5 10

<210> 15  
 <211> 48  
 <212> DNA  
 <213> Mouse

<400> 15  
 gtcaccaggc tcggttcctt cgggtcccat ctctactcgt ctttcacc 48

<210> 16  
 <211> 15  
 <212> PRT  
 <213> Mouse

<400> 16

Val Val Arg Ala Lys Gly Ala Gln Gly Arg Asp Glu Gln Lys Val  
 1 5 10 15

<210> 17  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> PCR primer

<400> 17  
 agaagtgcac ccaggttggc 20

<210> 18  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>

<223> PCR primer

<400> 18  
ggaagagggg cgtcagcaat

20

<210> 19  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic peptide

<400> 19

Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg  
1 5 10 15

<210> 20  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic peptide

<400> 20

Ser Gln Pro Arg Lys Gly Arg Lys Pro Pro Ala Val Pro Lys  
1 5 10

<210> 21  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> B127FR4-29 primer for PCR

<400> 21  
gctctggatg gcctactgc

19

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> B127FR4-17 primer for PCR

<400> 22  
agaagtgcac ccaggttggc

20

<210> 23  
<211> 19  
<212> DNA

<213> Artificial Sequence

<220>

<223> B127FR4-33 primer for PCR

<400> 23

gtgtgctcgc tcagaaggg

19

<210> 24

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward primer Mforw4 for PCR

<400> 24

tggcaggtgg ggatggaa

18

<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer Mrev15 for PCR

<400> 25

ggaggggatgg aaggggagga

20

<210> 26

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward primer Mforw2 for PCR

<400> 26

tcccacctga agactaagc

19

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer Mrev32 for PCR

<400> 27

tcacagctct ctggacagaa

20

<210> 28

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer B127FR4-21 for PCR

<400> 28

ggcttctgag gctgcacc

18

<210> 29

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Double-paired finger motif

<400> 29

Cys Cys Cys Cys His Cys Cys Cys

1

5

<210> 30

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Structural motiff

<220>

<221> MISC\_FEATURE

<222> (1)..(42)

<223> Xaa is any amino acid

<400> 30

Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys

1

5

10

15

Xaa Xaa Xaa Xaa His Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

20

25

30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys

35

40